SEQUENCE LISTING

```
CUSIN; Isabelle
<120> SECRETED POLYPEPTIDE SPECIES ASSOCIATED
  WITH CARDIOVASCULAR DISORDERS
<130> DV/4-33628A/GEP US-P
<140> 10/561,292
<141> 2005-12-20
<150> 60/484,153
<151> 2003-06-30
<150> PCT/EP2004/007047
<151> 2004-06-29
<160> 8
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 456
<212> PRT
<213> Homo sapiens
<220>
<221> PROPEP
<222> (1)...(456)
<223> Precursor protein of CP22
Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly
                5
                                    10
Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu
            20
                                25
Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr
                            40
                                                45
Gly Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys
                        55
Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His
                                        75
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys
                                    90
Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys
            100
                                105
Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro
                            120
                                                125
Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro
                        135
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Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro

Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Gln Gln

150

140

155

<110> BOUGUELERET; Lydie

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Gln Glu His Leu Leu Gly Asp Leu Gln Asn Asp Val His Arg Val Ala
                               185
Asp Ser Leu Pro Gly Leu Trp Lys Ala Leu Pro Gly Asn Leu Thr Ala
                            200
Ala Ser Leu Ser Asn Asp Val Lys Asn Val Gly Arg Cys Cys Glu Ala
                        215
                                            220
Glu Ala Gly Ala Gly Ala Ala Ser Leu Asn Ala Ser Leu His Gly Leu
                                       235
                    230
His Asn Ala Leu Phe Ala Thr Gln Arg Ser Leu Glu Gln His Gln Arg
               245
                                    250
Leu Phe His Ser Leu Phe Gly Asn Phe Gln Gly Leu Met Glu Ala Asn
                                265
Val Ser Leu Asp Leu Gly Lys Leu Gln Thr Met Leu Ser Arg Lys Gly
                            280
                                                285
Lys Lys Gln Gln Lys Asp Leu Glu Ala Pro Arg Lys Arg Asp Lys Lys
                        295
Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
                                        315
                    310
Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
                                    330
                325
Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
                                345
            340
Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
                            360
Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
                                             380
                        375
Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
                                        395
                    390
Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
                                     410
                405
Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
                                                     430
                                425
            420
Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
                            440
Gly Gly Phe Leu Met Phe Lys Thr
    450
<210> 2
<211> 433
<212> PRT
<213> Homo sapiens
<220>
 <221> PEPTIDE
 <222> (1)...(433)
 <223> Polypeptide sequence of SEQ ID NO:1 after removal
      of the signal peptide
 Ala Ser Ser Thr Ser Leu Ser Asp Leu Gln Ser Ser Arg Thr Pro Gly
                                     10
 Val Trp Lys Ala Glu Ala Glu Asp Thr Ser Lys Asp Pro Val Gly Arg
                                 25
 Asn Trp Cys Pro Tyr Pro Met Ser Lys Leu Val Thr Leu Leu Ala Leu
                             40
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170

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Cys Lys Thr Glu Lys Phe Leu Ile His Ser Gln Gln Pro Cys Pro Gln
Gly Ala Pro Asp Cys Gln Lys Val Lys Val Met Tyr Arg Met Ala His
                                        75
Lys Pro Val Tyr Gln Val Lys Gln Lys Val Leu Thr Ser Leu Ala Trp
                                    90
Arg Cys Cys Pro Gly Tyr Thr Gly Pro Asn Cys Glu His His Asp Ser
                               105
Met Ala Ile Pro Glu Pro Ala Asp Pro Gly Asp Ser His Gln Glu Pro
                           120
Gln Asp Gly Pro Val Ser Phe Lys Pro Gly His Leu Ala Ala Val Ile
                       135
                                            140
Asn Glu Val Glu Gln Gln Glu Gln Glu His Leu Leu Gly Asp
                   150
                                       155
Leu Gln Asn Asp Val His Arg Val Ala Asp Ser Leu Pro Gly Leu Trp
               165
                                   170
Lys Ala Leu Pro Gly Asn Leu Thr Ala Ala Ser Leu Ser Asn Asp Val
           180
                                185
Lys Asn Val Gly Arg Cys Cys Glu Ala Glu Ala Gly Ala Gly Ala Ala
                           200
Ser Leu Asn Ala Ser Leu His Gly Leu His Asn Ala Leu Phe Ala Thr
                       215
Gln Arg Ser Leu Glu Gln His Gln Arg Leu Phe His Ser Leu Phe Gly
                   230
                                        235
Asn Phe Gln Gly Leu Met Glu Ala Asn Val Ser Leu Asp Leu Gly Lys
               245
                                   250
Leu Gln Thr Met Leu Ser Arg Lys Gly Lys Lys Gln Gln Lys Asp Leu
           260
                                265
Glu Ala Pro Arg Lys Arg Asp Lys Lys Glu Ala Glu Pro Leu Val Asp
                           280
Ile Arg Val Thr Gly Pro Val Pro Gly Ala Leu Gly Ala Ala Leu Trp
                       295
                                            300
Glu Ala Gly Ser Pro Val Ala Phe Tyr Ala Ser Phe Ser Glu Gly Thr
                   310
                                        315
Ala Ala Leu Gln Thr Val Lys Phe Asn Thr Thr Tyr Ile Asn Ile Gly
                325
                                    330
Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Glu Arg Gly
                                345
Val Tyr Leu Phe Ala Val Ser Val Glu Phe Gly Pro Gly Pro Gly Thr
                           360
Gly Gln Leu Val Phe Gly Gly His His Arg Thr Pro Val Cys Thr Thr
                       375
                                           380
Gly Gln Gly Ser Gly Ser Thr Ala Thr Val Phe Ala Met Ala Glu Leu
                                       395
Gln Lys Gly Glu Arg Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr
               405
                                   410
Lys Arg Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
                                425
Thr
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<210> 3

<211> 152

<212> PRT

<213> Homo sapiens

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<220>
<221> PEPTIDE
<222> (1)...(152)
<223> Cardiovascular disorder Plasma Polypeptide 22 (CPP
<400> 3
Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
                                     10
Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
                             40
Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
            100
                                                     110
Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
        115
                            120
Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
                        135
Gly Gly Phe Leu Met Phe Lys Thr
<210> 4
<211> 24
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1)...(24)
<223> Tryptic peptides of CPP 22 found by MS-MS mass
      spectrometry in plasma samples of individuals with
      coronary artery disease
<400> 4
Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr Val
                 5
                                                         15
Phe Ala Met Ala Glu Leu Gln Lys
            20
<210> 5
<211> 12
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1)...(12)
<223> Tryptic peptides of CPP 22 found by MS-MS mass
```

spectrometry in plasma samples of individuals with coronary artery disease

```
Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr Lys
<210> 6
<211> 14
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1)...(14)
<223> Tryptic peptides of CPP 22 found by MS-MS mass
      spectrometry in plasma samples of individuals with
      coronary artery disease
<400> 6
Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
<210> 7
<211> 1371
<212> DNA
<213> Homo sapiens
<220>
<221> variation
<222> (1) ... (1371)
<223> Splice variant of the Endoglyx-1 gene and
      comprises the cDNA coding sequence for SEQ ID NO:
atgatectga gettgetgtt eageettggg ggeeceetgg getggggget getgggggea 60
tgggcccagg cttccagtac tagcctctct gatctgcaga gctccaggac acctggggtc 120
tggaaggcag aggctgagga caccggcaag gaccccgtag gacgtaactg gtgcccctac 180
ccaatgtcca agctggtcac cttactagct ctttgcaaaa cagagaaatt cctcatccac 240
togcagcago ogtqtoogca gggagotoca gactgocaga aagtcaaagt catgtacogo 300
atggcccaca agccagtgta ccaggtcaag cagaaggtgc tgacctcttt ggcctggagg 360
tgctgccctg gctacacggg ccccaactgc gagcaccacg attccatggc aatccctgag 420
cctgcagatc ctggtgacag ccaccaggaa cctcaggatg gaccagtcag cttcaaacct 480
ggccaccttg ctgcagtgat caatgaggtt gaggtgcaac aggaacagca ggaacatctg 540
ctgggagate tecagaatga tgtgeacegg gtggeagaea geetgeeagg eetgtggaaa 600
gccctgcctg gtaacctcac agctgcaagc ctgagcaacg acgtcaagaa tgtcgggcgg 660
tgctgcgagg ccgaggccgg ggccggggcc gcctccctca acgcctccct tcacggcctc 720
cacaacgcac tettegecac teagegcage ttggagcage accagegget ettecacage 780
ctctttggga acttccaagg gctcatggaa gccaacgtca gcctggacct ggggaagctg 840
cagaccatgc tgagcaggaa agggaagaag cagcagaaag acctggaagc tccccggaag 900
agggacaaga aggaagcgga gcctttggtg gacatacggg tcacagggcc tgtgccaggt 960
gccttgggcg cggcgctctg ggaggcagga tcccctgtgg ccttctatgc cagcttttca 1020
gaagggacgg ctgccctgca gacagtgaag ttcaacacca catacatcaa cattggcagc 1080
agctacttcc ctgaacatgg ctacttccga gcccctgagc gtggtgtcta cctgtttgca 1140
```

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gtgagcgttg aatttggccc agggccaggc accgggcagc tggtgtttgg aggtcaccat 1200
cggactccag tctgtaccac tgggcagggg agtggaagca cagcaacggt ctttgccatg 1260
gctgagctgc agaagggtga gcgagtatgg tttgagttaa cccagggatc aataacaaag 1320
agaagcctgt cgggcactgc atttgggggc ttcctgatgt ttaagacctg a
<210> 8
<211> 417
<212> PRT
<213> Mus musculus
<220>
<221> PEPTIDE
<222> (1)...(417)
<223> Q8K1Z7, a murine homologue of SEQ ID NO:1
Met Ile Pro Thr Leu Leu Gly Phe Gly Val Tyr Leu Ser Trp Gly
Leu Leu Gly Ser Trp Ala Gln Asp Pro Gly Thr Lys Phe Ser His Leu
Asn Arg Pro Gly Met Pro Glu Gly Trp Arg Leu Gly Ala Glu Asp Thr
                            40
Ser Arg Asp Pro Ile Arg Arg Asn Trp Cys Pro Tyr Gln Lys Ser Arg
Leu Val Thr Phe Val Ala Ala Cys Lys Thr Glu Lys Phe Leu Val His
                    70
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Gly Val Arg
                                     90
Val Met Tyr Arg Val Ala Gln Lys Pro Val Tyr Gln Val Gln Gln Lys
            100
                                105
Val Leu Ile Ser Val Asp Trp Arg Cys Cys Pro Gly Phe Gln Gly Pro
        115
                            120
                                                125
Asp Cys Gln Asp His Asn Pro Thr Ala Asn Pro Glu Pro Thr Glu Pro
                        135
                                            140
Ser Gly Lys Leu Gln Glu Thr Trp Asp Ser Met Asp Gly Phe Glu Leu
                    150
                                        155
Gly His Pro Val Pro Glu Phe Asn Glu Ile Lys Val Pro Gln Glu Gln
                165
                                    170
Gln Glu Ile Arg Arg Leu Ser Ser Asp Val Lys Gln Ile Gly Gln Cys
            180
                                185
                                                    190
Cys Glu Ala Ser Trp Ala Ala Ser Leu Asn Ser Ser Leu Glu Asp Leu
        195
                            200
His Ser Met Leu Leu Asp Thr Gln His Gly Leu Arg Gln His Arg Gln
                        215
                                            220
Leu Phe His Asn Leu Phe Gln Asn Phe Gln Gly Leu Val Ala Ser Asn
                    230
                                        235
Ile Ser Leu Asp Leu Gly Lys Leu Gln Ala Met Leu Ser Lys Lys Asp
                245
                                    250
Lys Lys Gln Pro Arg Gly Pro Gly Glu Ser Arg Lys Arg Asp Lys Lys
                                265
Gln Val Val Met Ser Thr Asp Ala His Ala Lys Gly Leu Glu Leu Trp
                            280
Glu Thr Gly Ser Pro Val Ala Phe Tyr Ala Gly Ser Ser Glu Gly Ala
                        295
                                            300
Thr Ala Leu Gln Met Val Lys Phe Asn Thr Thr Ser Ile Asn Val Gly
                    310
                                        315
Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Lys Arg Gly
```

				325					330					335	
Val	Tyr	Leu	Phe 340	Ala	Val	Ser	Ile	Thr 345	Phe	Gly	Pro	Gly	Pro 350	Gly	Met
Gly	Gln	Leu 355	Val	Phe	Glu	Gly	His 360	His	Arg	Val	Pro	Val 365	Tyr	Ser	Thr
Glu	Gln 370	Arg	Gly	Gly	Ser	Thr 375	Ala	Thr	Thr	Phe	Ala 380	Met	Val	Glu	Leu
Gln 385	Lys	Gly	Glu	Arg	Ala 390	Trp	Phe	Glu	Leu	Ile 395	Gln	Gly	Ser	Ala	Thr 400
Lys	Gly	Ser	Gln	Pro 405	Gly	Thr	Ala	Phe	Gly 410	Gly	Phe	Leu	Met	Phe 415	Lys
Thr														_	

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